

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2001, 14:25:52 ; Search time 2462.53 Seconds
(without alignments)
1738.920 Million cell updates/sec

Title: US-09-784-340-3_COPY_18322_18774

Perfect score: 453
Sequence: 1 gtaagtactactgtgtgtac.....tggtgttttccttcacg 453

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1022815 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
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257: gb_est177:*
258: gb_est178:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 4
LOCUS B80712
DEFINITION C17-HSP-2050M23.TR C17-HSP Homo sapiens genomic clone 2050M23. DNA
SEQUENCE
ACCESSION B80712 444 bp DNA GSS 24-OCT-1998
VERSION B80712
KEYWORDS B80712.1 GI:2867735
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 444)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K.,
Simon,M., and Venter,J.C.
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
Unpublished (1998)
Other_GSS: C17-HSP-2050M23.TR
JOURNAL
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..444
/organism="Homo sapiens"
/db_xref="GDB:7056598"
/db_xref="taxon:9606"
/clone="2050M23"
/clone_1lb="C17-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelBAC11; site_1: HindIII; site_2:
HindIII"

BASE COUNT 124 a 110 c 71 g 139 t
ORIGIN

Query Match 51.4%; Score 233; DB 257; Length 444;
Best Local Similarity 100.0%; Pred. No. 3.6e-44;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 aagctttattacatcttaatttaccacatttgttaagaatatactcttcaagtc 280
|||||
DB 54 AACCTTTATTACACTTATTTTACCCCATTTTGTAGAAATATCTCTTTCAGTCTC 113
|||||

QY 281 tccacatactctgttaatactatgttaaccacaataatctatgtcaacaaccagatcaat 340
|||||
DB 114 TCCACTATATCTGTTTAATATCTATGTAAACCAACAAATTTATGTCAACACAGATCAAT 173
|||||

QY 341 cttctactgaacatgtctctggtcttgacataacatactacggtttactacgtctctt 400
|||||
DB 174 CTTTACTGACATGTTCTTGCGCTTGCAATATACATATACAGGTTTATCTACGTTCTTT 233
|||||

QY 401 tatgaaacaaactaacaacttcttaagttctatgtgtgtttccctccag.453
|||||
DB 234 TATGAAACAAACTACAACTTCTAAGTCTATAGTGTGTTTCCCTTCAG 286
|||||

RESULT 5
LOCUS AQ106323/c 335 bp DNA GSS 28-AUG-1998
DEFINITION HS_3056_A2_D08_MF C17 Approved Human Genomic Sperm Library D Homo

ACCESSION sapiens genomic clone Plate=3056 Col=16 Row=G, DNA sequence.
LOCUS AQ106323 335 bp DNA GSS 28-AUG-1998
DEFINITION HS_3056_A2_D08_MF C17 Approved Human Genomic Sperm Library D Homo

QY 30 taacattgactatgttatcatattataccagaataatgttaa:atcatccctggttagaatg 89
|||||
DB 315 TACCATGAGTATGTTTATA-ATCATCTAGAGATGTCAG-3GCCATPACATGAGACTAT 257
|||||

QY 90 ttgaggaatttactccacaataatgagtcattcatcacc:tgtagctggaatagtg 149
|||||
DB 256 ATAAAGATATTCCTCCCTCAATTCACAGTCAATTTATATC TACCATTGCA--AGTCTG 199
|||||

QY 150 gaattgtagtcatagagtggtcaaatcttcttcattgaagaa:cataggttaagttaaca 209
|||||
DB 198 GAAATGTAATGATAGAGTCAATCTCTTCTTGAA:ACTAGATTAAATTAAGG 139
|||||

QY 210 acggtctactaagctttatcatcattcaatcttcccatctt--tgttaagaataata 267
|||||
DB 138 ACCAGCTTACTAAGTATTTTCTATGTCCTCATTTTACCCTCTGTGATTAAGAAATGCTT 79
|||||

QY 268 ctctttagctctccacatatactgtttaatactatgta:ccacaataatctagtcac 327
|||||
DB 78 CTTTTTAATTTGCGCCACTGTAAGCTTTCACTGATGATGCA:CAACAAGATTATATACAC 19
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QY 328 aaccagaatcaatcttt 345
|||||
DB 18 AACAAAGATCTATCTTTT 1
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RESULT 6
LOCUS CNS0039G 1101 bp DNA GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey s:quence TET3 end of BAC #

FEATURES
source
Location/Qualifiers
1..335
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3056 Col=16 Row=3"
/clone_1lb="C17 Approved Human Genomic Sperm Library D"
/sex="Male"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"

BASE COUNT 113 a 50 c 69 g 103 t
ORIGIN

Query Match 28.9%; Score 130.8; DB 224; Length 335;
Best Local Similarity 69.5%; Pred. No. 1.6e-20;
Matches 221; Conservative 0; Mismatches 12; Indels 5; Gaps 3;

QY 30 taacattgactatgttatcatattataccagaataatgttaa:atcatccctggttagaatg 89
|||||
DB 315 TACCATGAGTATGTTTATA-ATCATCTAGAGATGTCAG-3GCCATPACATGAGACTAT 257
|||||

QY 90 ttgaggaatttactccacaataatgagtcattcatcacc:tgtagctggaatagtg 149
|||||
DB 256 ATAAAGATATTCCTCCCTCAATTCACAGTCAATTTATATC TACCATTGCA--AGTCTG 199
|||||

QY 150 gaattgtagtcatagagtggtcaaatcttcttcattgaagaa:cataggttaagttaaca 209
|||||
DB 198 GAAATGTAATGATAGAGTCAATCTCTTCTTGAA:ACTAGATTAAATTAAGG 139
|||||

QY 210 acggtctactaagctttatcatcattcaatcttcccatctt--tgttaagaataata 267
|||||
DB 138 ACCAGCTTACTAAGTATTTTCTATGTCCTCATTTTACCCTCTGTGATTAAGAAATGCTT 79
|||||

QY 268 ctctttagctctccacatatactgtttaatactatgta:ccacaataatctagtcac 327
|||||
DB 78 CTTTTTAATTTGCGCCACTGTAAGCTTTCACTGATGATGCA:CAACAAGATTATATACAC 19
|||||

QY 328 aaccagaatcaatcttt 345
|||||
DB 18 AACAAAGATCTATCTTTT 1
|||||

melanogaster genome using these BACs. For further information please see [http://www.fruitfly.org/The BDPG Drosophila melanogaster BAC library](http://www.fruitfly.org/The%20BDGP%20Drosophila%20melanogaster%20BAC%20library) was prepared by Kazutoyo Oseegawa and Aaron Mammaster in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDPG from the isogenic strain y2: cn bw^{sp}, the same strain used for the BDPG's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://dbacpac.med.buffalo.edu/drosophila_bac.htm.

RESULT	15
CNS017YY/c	
LOCUS	CNS017YY 1101 bp DNA GSS 26-JUL-1999
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC BACN3J7808 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL108676
VERSION	AL108676.1 GI:5628980
KEYWORDS	GSS.
SOURCE	Fruit fly.
ORGANISM	Plasmid Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 1101)
REFERENCE	Genoscope.
AUTHORS	Direct Submission
TITLE	

QY	39	ctatgctatcatattacccagaacatgctaaatcatccctcctgtagcaatgcttggagggat	98
Db	1059	CTCTGCTATCATATTACCCAGAACATGCTAAATCATCCCTCTGTAGCAATGCTTGGAGGGAT	1000
QY	99	tttaccacaataatctatgactatctacaaactgttaccctcctacatgcttctggaatctga	158
Db	999	TTTACCACAATAATCTATGACTATCTACAAACTGTTACCCTCTACATGCTTCTGGAATCTGA	940
QY	159	gttcaatagatgttcaaaactctcttcataggaatataagcttaagatcaaacatgcttta	218
Db	939	GTTCAATAGATGTTCAAAACTCTCTTCTCATAGGAATATAAGCTTAAATCAAACTGTTTA	880
QY	219	ctaagctttatcatcaactcctaaatttaaccccatcttctttaaagaataatccttaagtc	278
Db	879	CTAAGCTTTATCATCAACTCCTAAATTTAACCCCATCTTCTTTAAAGAATAATCCTTAAGTC	820
QY	279	ttctccaatatcatcgttcttaatactatgtaacaaacaatatctatgtaacaaacaagatca	338
Db	819	TTCTCCAAATCATCGTTCTTAATACTATGTAACAAACAATATCTATGTAACAAACAAGATCA	761
QY	339	atcctttactgaacatgctctctgcttgctgaataacatatacctacggatcttatacgaatgct	398
Db	760	ATCCTTTACTGAACATGCTCTCTGCTTGCTGGAATAACATATACCTACGGATCTTATACGAATGCT	701
QY	399	tttatgaaacaacaaactacaactcttctaagttctatgctctcttcttcscct	449
Db	700	TTTATGAAACAACAACAACTACAACCTCTTCTAAGTTCTATGCTCTCTTCTTCTTCTTCTTCTTCT	650

Search completed: August 27, 2001, 17:07:35
Job time: 9703 sec

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